

Figure 1A

SEQ ID NO:1

/translation="MGSVLSTDSGKSAPASATARALERRRDPELPVTSFDCAVCLEVL HQPVRTRCGHVFCRSCIATSLKNNKWTCPYCRAYLPSEGVPATDVAKRMKSEYKNCAE CDTLVCLSEMRAHIRTCQKYIDKYGPLQELEETAARCVCPFCQRELYEDSLLDHCITH HRSERRPVFCPLCRLIPDENPSSFSGNLIRHLQVSHTLFYDDFIDFNIIEEALIRRVLDRSLLEYVNHSNTT"

## Figure 1B

## SEQ ID NO:2

AGCGGAGGTCATTTTTGCAGCTTATTGTGATGACAACAGTGGAGGATGGTCTTCCACTTCA CCTTAAAAGCGGCTGTTCTCTGATTATCATTAAGCATGGCCACGCCCGCACTTAACTTCTG ACAGTGGGGAAAGCAGCTGTGTGTGATAGCTTGGAAGGTTTACTGCTGCCTCAAGTCCTCT TCTCTGCAGTTGAGGTTTCAGGTTTCAATCCTCCCAATACCACAAGACAGAGCACGGGGCG GCTGCCGCCTCCGCCCCTTAACCTAGGCGGCTTGCCGAAGATCTCAGCCCCGCGG CCGCGCGCTCGCCTAGACCAGGGTTGGGCGCAGCGGCGAGGTGGCTTCTGGGCT CGCACGCAACAAAACAACCTGCGGCAGGCACTGAGTGCTTCGCAGCTGTCTGGGCGAGA GGCACAGCGATGGGCTCCGTGCTGAGCACCGACAGCGGCAAATCGGCGCCCCCCCTCTGCCA  $\verb|CCGCGCGGGCCCTGGAGCGCAGGAGGGACCCGGAGTTGCCCGTCACGTCCTTCGACTGCGC|\\$ CGTGTGCCTTGAGGTGTTACACCAGCCTGTCCGGACCCGCTGCGGCCACGTATTCTGCCGT TCCTGTATTGCTACCAGTCTGAAGAACAACAAGTGGACCTGTCCTTATTGCCGGGCATATC TTCCTTCAGAAGGAGTTCCAGCAACTGATGTAGCCAAAAGAATGAAATCAGAGTATAAGAA CTGCGCTGAGTGTGACACCCTGGTTTGCCTCAGTGAAATGAGGGCACATATTCGGACTTGT CAGAAGTACATAGATAAGTATGGACCACTACAAGAACTTGAGGAGACAGCAGCAAGGTGTG TATGTCCCTTTTGTCAGAGGGAACTGTATGAAGACAGCTTGCTGGATCATTGTATTACTCA TCACAGATCGGAACGGAGGCCTGTGTTCTGTCCACTTTGCCGTTTAATACCCGATGAGAAT CCAAGCAGCTTCAGCGGCAATTTAATAAGACATCTGCAAGTTAGTCACACTTTGTTTTATG ATGATTCATAGATTTTAATATAATTGAGGAAGCTCTTATCCGAAGAGTCTTAGACCGGTC ACTTCTTGAATATGTGAATCACTCGAACACCACATAATTTTATTAAAACGAAGGGAAAAGG TTGATGGGCAAAAATGTACAACACAGTTATGTGTTTTGTCCATGTTTATTGTTATAGTGCAT TTAAAAACTGCTTTAATTTTTAATGGTTTAAATCTGTTTTACATCCTTGAGATTCTTACACA TCTAACAACAAAAAAATTATCTACATCAGTCATTGTTACATGGAAAAGACAGGTGGTAGG CAAGTAGGTGGAGGATCTCGGTTTGCAAATTAGATAATACTCTGTGTATAATGCTACATAT AGAGTGAAACAAAGTGCAGACATTCAAAGAAATAAGAAATCTGCTCCAATGCTCTTGTTCT AATCTCTAATAGGTTAACGTTAATAATCTTGTATGGGAGTTGGAAAGGAAAATTTTGGAAG TCAAGAAAGTCCATTTAGGCCGGACGCGGTGGCTTACGCTTGTAGTCCCAGCACTTTGGGA GGCTGAGGCAGGCGGATCACAGGGTCGGGAGTTCGAGACCAGCCTGGCCAACACTGGTCTC TGTGAAACTCCGTCTCTACTGAAAATGCAAAGATTGGCTGGACGTGTTGGCGGGCATCTGT GATACCAGCTACTTGGGAGGCTGAGGCAGAAGAATCGCTTGAGCCCGGGAGGCGGAGGTTG CAGTGAGCTGAGATCGCGCCAGTACACTCCAGCCTGGGTAACAGAGCTAGACTCCATCTCA AAAAAAAAAAAAAAA

in and the sine was read that interesting an interest form for a minimum and extended sound of the first ended and

## Figure 1C

## SEQ ID NO:3

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1 acttctgaca gtggggaaag cagctgtgtg tgatagcttg gaaggtttac tgctgcctca
 61 agtectette tetgeagttg aggttteagg ttteaateet eccaatacea caagacagag
121 caeggggegg etgeegeete egeeteegeg eettaaceta ggeggettge egaagatete
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301 teetteetee acegeaegge aacaaaacaa eeetgeggea ggeaetgagt gettegeage
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## Figure 1D

## SEQ ID NO:4

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## Figure 1E

SEQ ID NO:5

## TRAC1 genomic region:

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Managemental and a managemental construction of the contraction of the

ACTTCTGACAGTGGGGAAAGCAGCTGTGTGTGATAGCTTGGAAGGTTTACTGCTGCCTCAA GTCCTCTCTCTGCAGTTGAGGTTTCAGGTTTCAATCCTCCCAATACCACAAGACAGAGCA CGGGGCGCTGCCGCCTCCGCCCTTAACCTAGGCGGCTTGCCGAAGATCTCAGC  $\verb|CCCGCGGCCGCGCGCTCGCCCTAGACCAGGGTTGGGCGCAGCGGCGGAGGTGGCTT| \\$ CTGGGCTGCGCGAGCTGGGAGAGCTGGGAGGCGGCGATCGCAGCTGGGCCGGGACTTCCTT CCTCCACCGCACGGCAACAAACAACCCTGCGGCAGGCACTGAGTGCTTCGCAGCTGTCTG TCTGCCACCGCGCGGCCCTGGAGCGCAGGAGGGACCCGGAGTTGCCCGTCACGTCCTTCG ACTGCGCCGTGTGCCTTGAGGTGTTACACCAGCCTGTCCGGACCCGCTGCGGCCACGTATT CTGCCGTTCCTGTATTGCTACCAGTCTAAAGAACAACAAGTGGACCTGTCCTTATTGCCGG GCATATCTTCCTTCAGAAGGAGTTCCAGCAACTGATGTAGCCAAAAGAATGAAATCAGAGT ATAAGAACTGCGCTGAGTGTGACACCCTGGTTTGCCTCAGTGAAATGAGGGCACATATTCG GACTTGTCAGAAGTACATAGATAAGTATGGACCACTACAAGAACTTGAGGAGACAGCAGCA AGGTGTGTATGTCCCTTTTGTCAGAGGGAACTGTATGAAGACAGCTTGCTGGATCATTGTA TTACTCATCACAGATCGGAACGGAGGCCTGTGTTCTGTCCACTTTGCCGTTTAATACCCGA TGAGAATCCAAGCAGCTTCAGTGGCAGTTTAATAAGACATCTGCAAGTTAGTCACACTTTG TTTTATGATGATTCATAGATTTTAATATAATTGAGGAAGCTCTTATCCGAAGAGTCTTAG ACCGGTCACTTCTTGAATATGTGAATCACTCGAACACCACATAATTTTATTAAAACGAAGG TCAATGATTGATGGGCAAAAATGTACAACACAGTTATGTGTTTTGTCCATGTTTATTGTTAT AGTGCATTTAAAAACTGCTTTAATTTTAATGGTTTAAATCTGTTTTACATCCTTGAGATTC TTACACATCTAACAACAAAAAAAATTATCTACATCAGTCATTGTTACATGGAAAAGACAGG TGGTAGGCAAGTAGGTGGAGGATCTCGGTTTGCAAATTAGATAATACTCTGTGTATAATGC TACATATCAATAACTACCATCATGGTTAGGCACGATAACTAATCTTTGTTCTGTGTAAAAA AATATGGAGAGTGAAACAAAGTGCAGACATTCAAAGAAATAAGAAATCTGCTCCAATGCTC TTGTTCTAATCTCTAATAGGTTAACGTTAATAATCTTGTATGGGAGTTGGAAAGGAAAATT TTGGAAGTCAAGAAAGTCCATTTAGGCCGGACGCGGTGGCTTACGCTTGTAATCCCAGCAC TTTGGGAGGCTGAAGCAGGCGGATCACAAGGTCAGGAGTTCGAGACCCAGCCTGGCCAACAC TGGTCTCTGTGAAACTCCGTCTCT

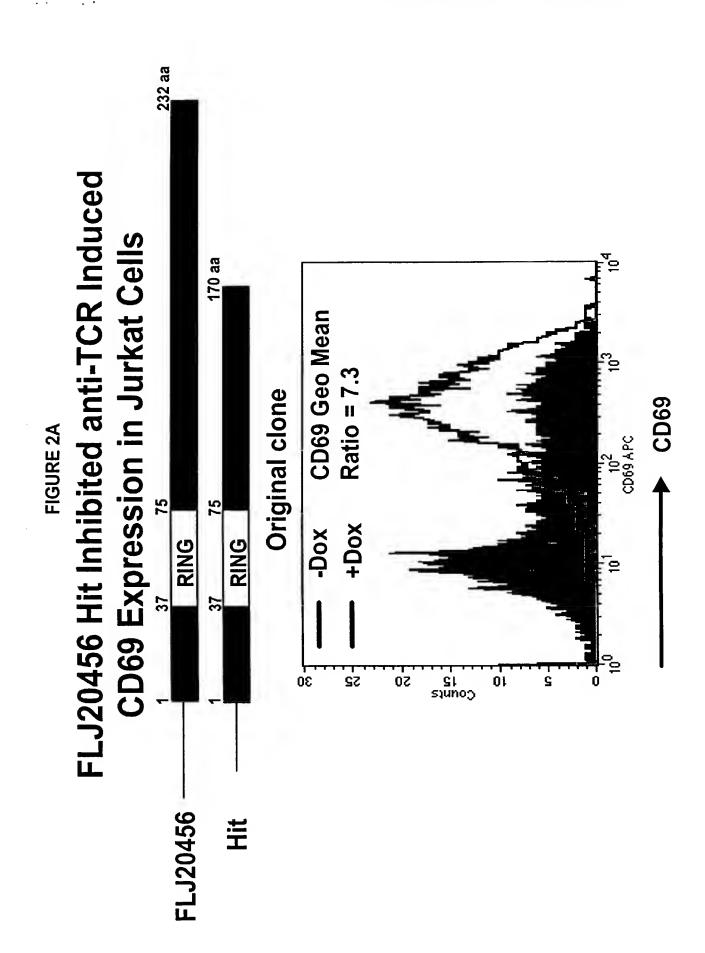
## Figure 1F

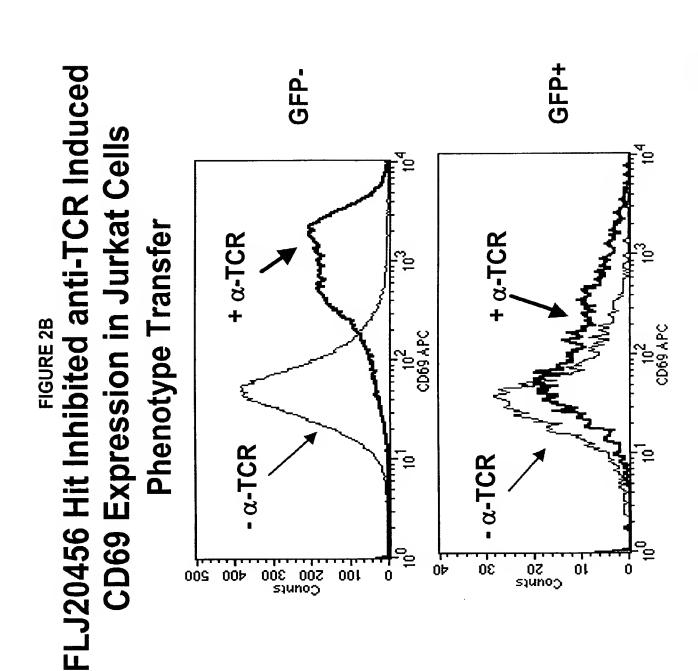
## SEQ ID NO:6 Mouse TRAC1 cDNA sequence:

GCGGGACAACAGAACCACCCGCAGCCAGCAGGGAGCTCCTGGCAGCTCGC TGAGCTAGAGCGCAAGNNTGGGCTCCCTGCTGAGCAGCGACAGCTCCAAG TCCGCGCCCGCCACCCCGCGGACTCTGGAGCGCAGCGGGGACTC GGAGCTGCCCATCACCTCCTTCGACTGCTCAGTGTGTCTGGAGGTGCTAC ACCAGCCGGTCCGGACCCGCTGTGGCCACGTGTTCTGCCGATCTTGCATT GCGACCAGTATAAAGAACAATAATAAATGGACATGTCCATACTGCCGGGC ATACCTTCCTTCAGAGGGAGTGCCCGCAACTGACATAGCCAAGAGGATGA AGTCAGAATACCAGAACTGTGCTGAGTGTGGAACTCTGGTTTGCCTCAGT GACATGAGGGCGCACATAAGGACCTGTGAGAAGTACATCGATAAATATGG CCCGCTGCTAGAACTTGGCGACACCACAGCAAGATGTGTATGTCCATTTT GTCAGCGGGAACTGGATGAAGACTGCTTGCTGGATCATTGCATTATCCAC CACAGATCAGAAAGGAGGCCCGTGTTCTGTCCACTTTGCCATTCACGACC TGATGAAAGCCCAAGTACCTTCAATGGCAGTTTAATTAGACATTTGCAAG TCAGTCACACTTTGTTTTATGATGATTTCATAGATTTTGATATAATTGAG GAAGCCATTATTCGCAGAGTGCTAGACCGCTCACTTCTTGAATATGTGAA TCAGTCAAACACCACATAATTTTATGACTAGGAAGGGGACCATTCACTCG TACCATTTAAGATGCTGCTTGAAGGACTGGAGGGGGATTGTCGACGTTTG ATGGAGAAACATGTACTACAGTATTACCTGCTTGTCTTTGTTATGTTGCA TTCAAAAACCGTGTTCATTCTGGCTTAGATCTGCCCTTACATTCTTGAGT CTATTAGACATTTAACCACGAGACACAGCCTCTCAGCCATTAACAGATGG AAGAGACACGACACGGCTGGCTATGTGATGGAGCAGCTTCCTGTGTCCA TTAGTGATGTGTGTATAACGCTACATATTCCCAACTGTCATCATGGTTAG GCGAGAAAGCCAATCTCTGTTCCATGCTAAAAGACGGAGAAAGGAACAAA ATATGGACATTAARGGAAATCTGAAATGTATTCAAATTCTCATGCTCTAA TCTCCAATAAGGAACGTGAATAATCTTATGAAAAGGAGGAAAGGGAAGAA TTTGAAGTCACCAAAATCCAATTTAGCCAAATTATAGTACATAATATAAT **ACTGCAGC** 

## SEQ ID NO:7 Mouse TRAC1 protein (3<sup>rd</sup> frame)

SAXXGSLLSSDSSKSAPASATPRTLERSGDSELPITSFDCSVCLEVLHQP VRTRCGHVFCRSCIATSIKNNNKWTCPYCRAYLPSEGVPATDIAKRMKSE YQNCAECGTLVCLSDMRAHIRTCEKYIDKYGPLLELGDTTARCVCPFCQR ELDEDCLLDHCIIHHRSERRPVFCPLCHSRPDESPSTFNGSLIRHLQVSH TLFYDDFIDFDIIEEAIIRRVLDRSLLEYVNQSNTTFYD





Full Length FLJ20456 Does Not Inhibit CD69 Upregulation in Jurkat Cells Figure 3A

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FLJ20456

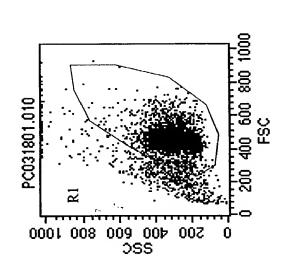
RING

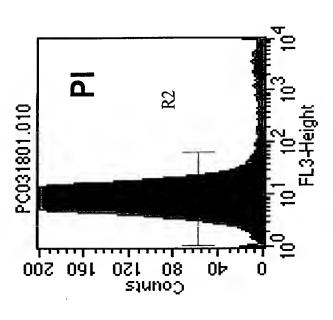
232 aa

Pfu PCR product amplified from a capped human brain cDNA library.

One N to S polymorphism with FLJ20456 NM\_017831.1 at amino acid 186, present in EST database.

## JurkatN 32H





Full Length FLJ20456 Does Not Inhibit CD69 Upregulation in Jurkat Cells

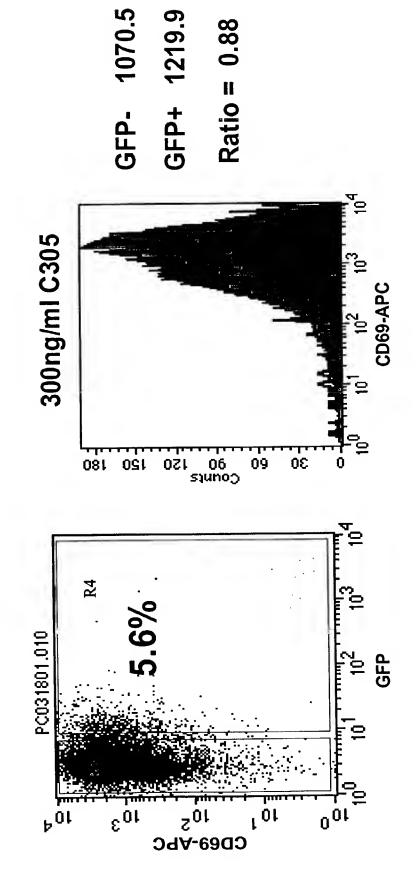
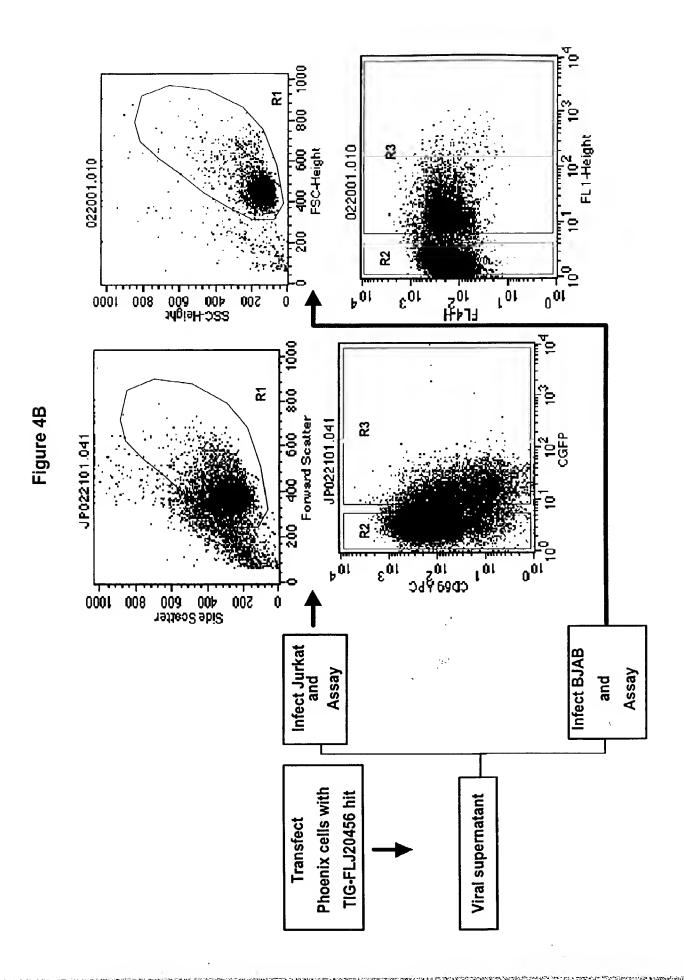


Figure 4A

1





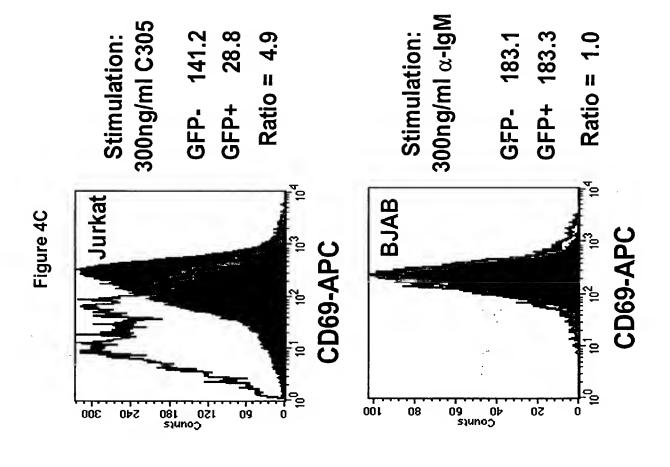
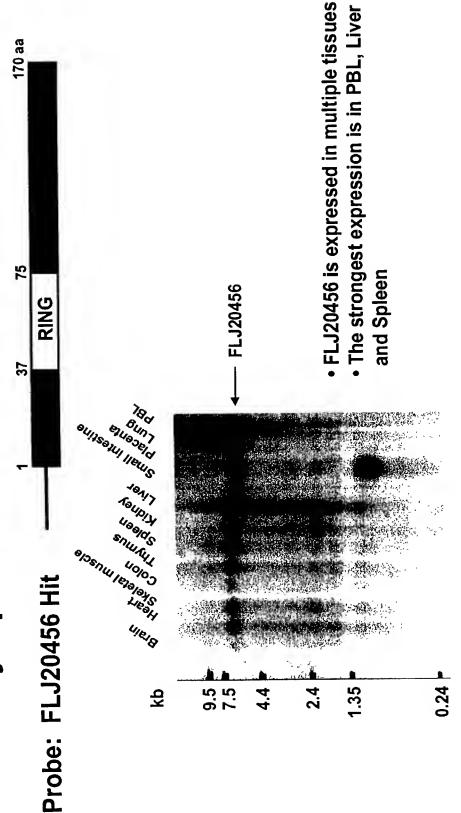
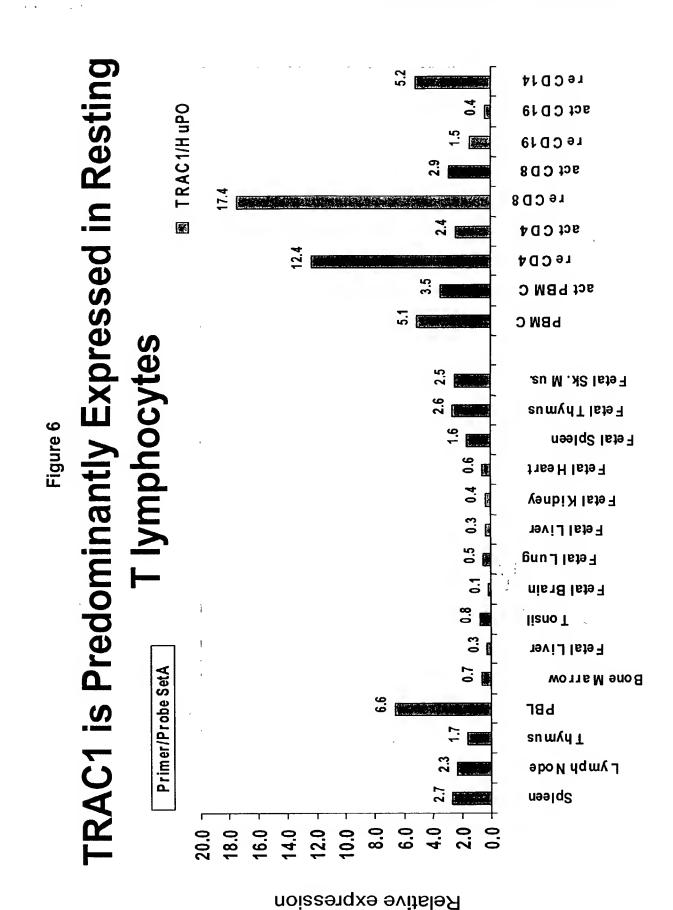


Figure 5

# FLJ20456 Is Strongly Expressed in Lymphoid and Hematopoietic Organs





# FL20456 Sequence is Most Similar to Two Sequences: Znf313 and STRIN

King Domain  1F.C.VC.EVPVC.HVFCC	FLJ20456.pep MGSVLSTDSGKSAPASATARALERRRDPELFVTSFDCAVCLEVIHQPVR-IRCGHVFCRSCIAISLKN 67 znf313.pepMAAQQRDCGCAAQLAGFAAEADFLGRFTCFVCLEVYEKPVQV-PCGHVFCSACLQECLKP 59 STRIN.pep	1CGRA	p nkwiceycrayldeseGveridoakrwkseykncaecdilvolsewrahiriockyidrygeloe 131 kkevcgvcrsalapGvraveleroiestetschocrkwfflskirshvancskyon-yimegv 121 sgahcelorovtrreracperaldenimrkfsgscrocakoikfiramrhyksckyodevgvssi 117	1hchchc	P LEETAAR	1 .V.CP.CPPNHYFEES	POFICELCRIIPDENPSSFSGNLIRHLOVSHTLFYDDFUDFNILEBALIRRVIDRSLLEYVNHSNTT. 233 SWWCPICASMPWGDPNYRSANFREHIGRRHRFSYDTFVDYDVDEEDMMNQVLORSIIDQ. 229 PWTCPICVSLPWGDPSQITRNFVSHLNORROEDMGEEWNLQIDEETQYQTAVEESFQVNI.
Consensus #1	FLJ20456.pep MC znf313.pep STRIN.pep	Consensus #1	FLJ20456.pep NE znf313.pep Ka	Consensus #1.	FLJ20456.pep LEETAAR- znf313.pep KATIKDAS STRIN.pep VPNFQISQ	Consensus #1.	FLJ20456.pep PWFCPL znf313.pep SWWCPL STRIN.pep PWICPL

_							
	26.6		134.7	2			
		130.4	140.9	1			
	-	2	3				
	* All three sequences are human	Murine sequences are not snown		7 213			

FLJ20456.pep znf313.pep

22.3

STRIN.pep

FIG. 7.

## Alignment of RING Domain Sequences from Various Human Proteins 50 50 50 LMCTSCLTSW--QESEGQGCPFCRCEI-KG IFCKFCMLKLLNQKKGPSQCPLCKNDITKR RHCLALWWA-SSKKTECHECKEK--WE FORVOILRCL--KVMGSYCPSCRYPCF-P SACLOECL--KPKKPVCGVCRSALA-P CFLTAM--RESGAHCPLCRGNV--T RECKACIIKSI--RDAGHKOPV-DNEILLE ...C.H..C...C MATH F/G. 8. STFOICKICHEN-DKDV ESKYECPICLMAL VSEFSCHCCMDIE FLJ20456 TRAF6 EDDFYCPV VISFDCAV LGRFTCPV VKSISC FLJ20456.Ring <del>|</del>| znf313.Ring STRIN. Ring TRAF6.Ring c-Cbl.Ring BRCA1.Ring Consensus RAG1.Ring BAR.Ring Cb1 **BRCA1** BARD1 RING RAG1

Figure 9

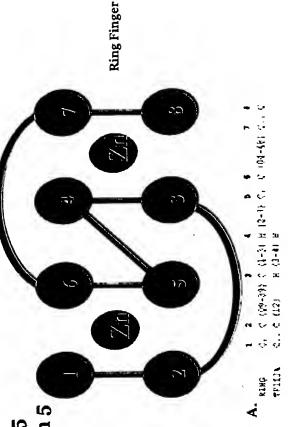
Kit.

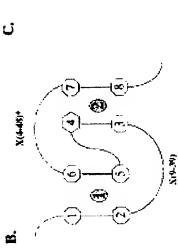
## RING finger vs. Zinc finger proteins

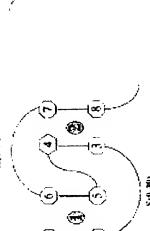
Ring H2: C<sub>3</sub>H2C<sub>3</sub> = His in position 5 Ring-HC:  $C_3HC_4 = Cys$  in position 5

ordinate two zinc atoms pattern of Cys and His to form a cross-brace Ring finger domains have a conserved residues that costructure

structurally distinct from Ring fingers are zinc fingers







## Figure 10A

## **Ubiquitin Pathway Components**

- E1: ubiquitin-activating enzyme, with a major isoform that may work broadly
- E2: ubiquitin-conjugating enzyme, a class of ~14 enzymes, interacts with E3
- activities that promote addition of ubiquitin to specific E3: ubiquitin ligases, a broad and growing group of proteins
- binding of substrates and a 20S catalytic core with three base that mediates ATP- and ubiquitin-chain-dependent Proteasome-a 26S complex containing a 19S lid and known proteolytic activities.

Figure 10B

## **Enzymology of Ubiquitination**

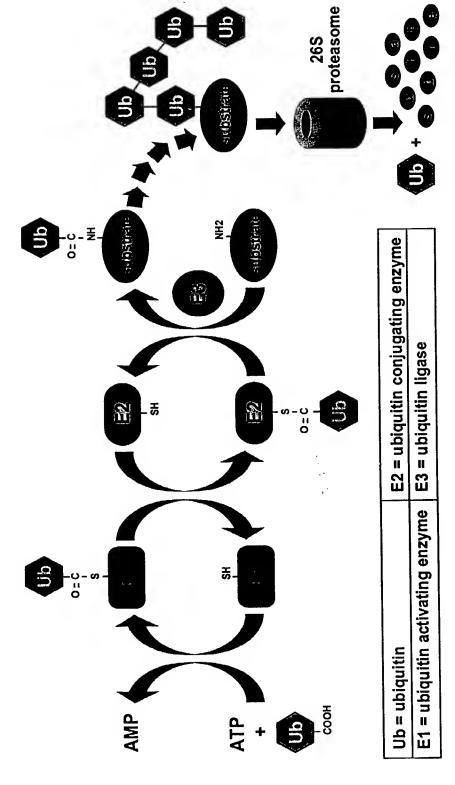
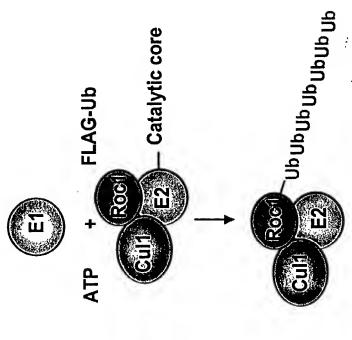


Figure 11A

Sandaras val.

## A Reconstituted, Substrate-independent Assay for Studying Ligase Catalysis



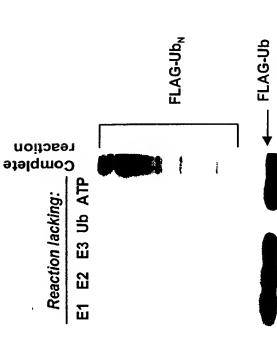
has the same catalytic properties and The substrate-independent reaction requirements for Roc1/Cul1 as the substrate-dependent reaction

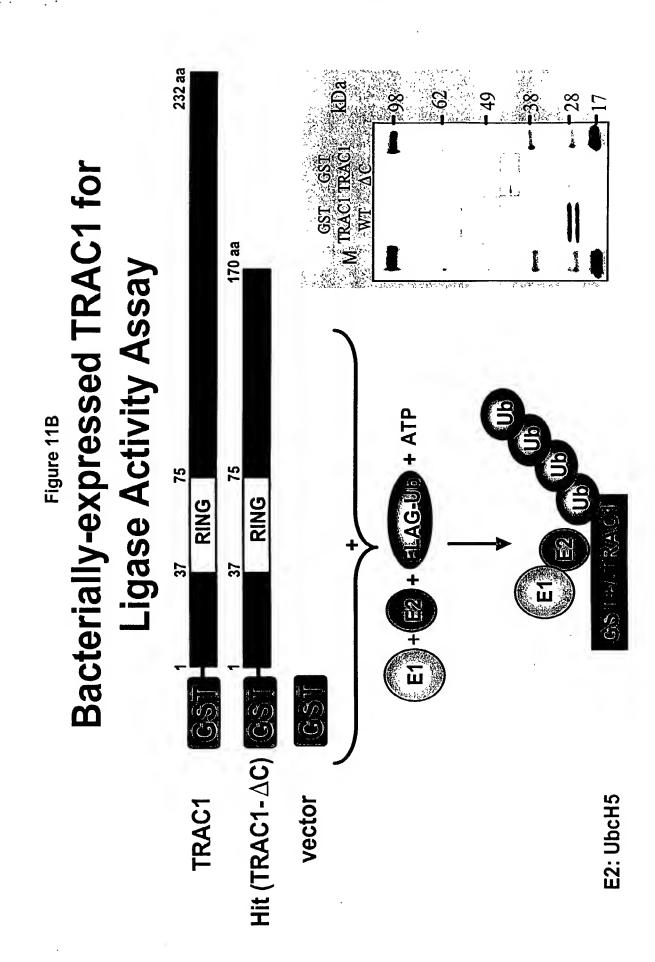
## Reaction Components

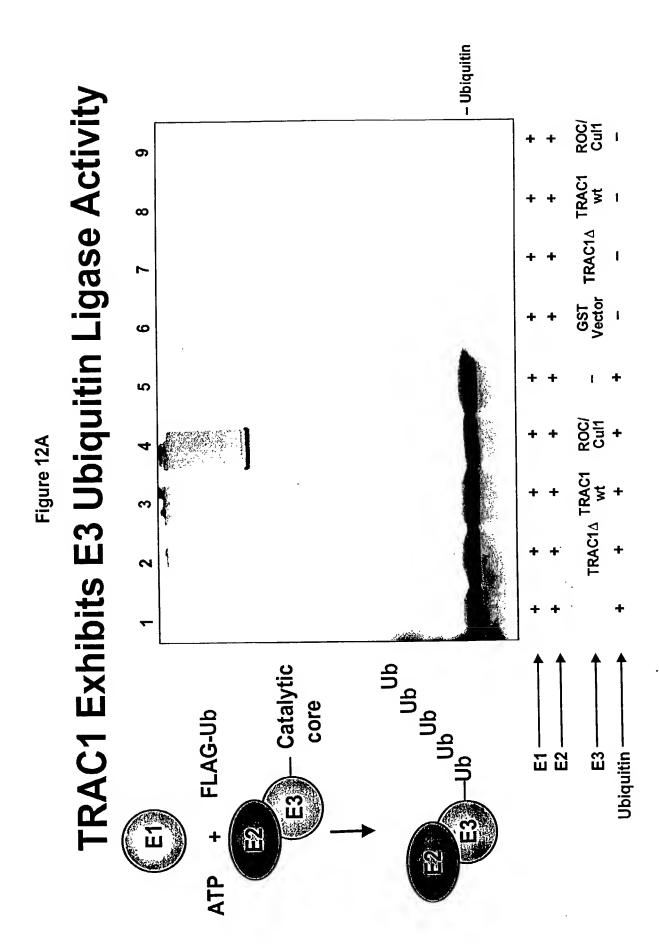
E2 (UbcH5): GST-fusion (cleaved), E.coli

E3 (Ring/cullin): His-tagged, coexpressed, baculovirus

Ubiquitin: FLAG-tagged, E.coli

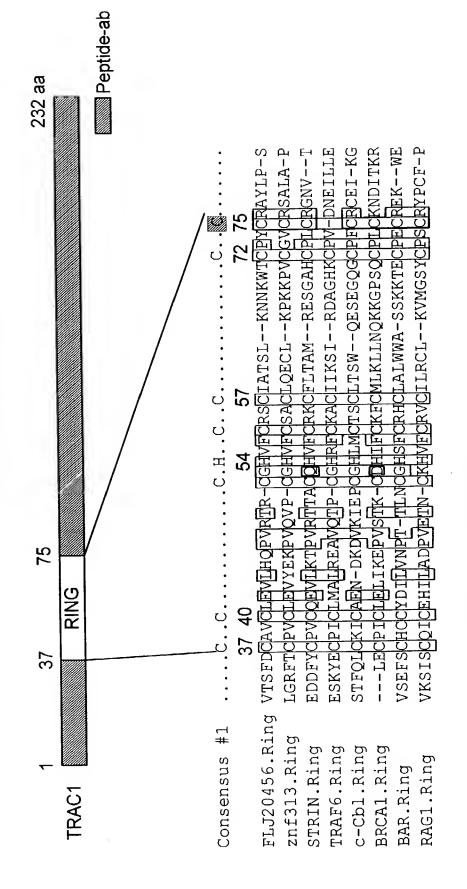






a-Flagar a-Flag Blot The Ring Domain is Required for TRAC1 Ligase Activity 232 aa Flag Flag 232 aa kDa Vector ∆76 7C WT Flag TRACI 170 aa ROC/Cal 1 Figure 12B 22 75 Flag-Ubiquitin → RING RING 37 37 Transfect PhoenixA cells TRAC1 TRAC1-?C **9**2V Ubiquitin ligase assay IP with α-Flag ab Cell lysates Wash 2x

Point mutations in Conserved Cysteine Residues of the TRAC1 Ring finger Domain

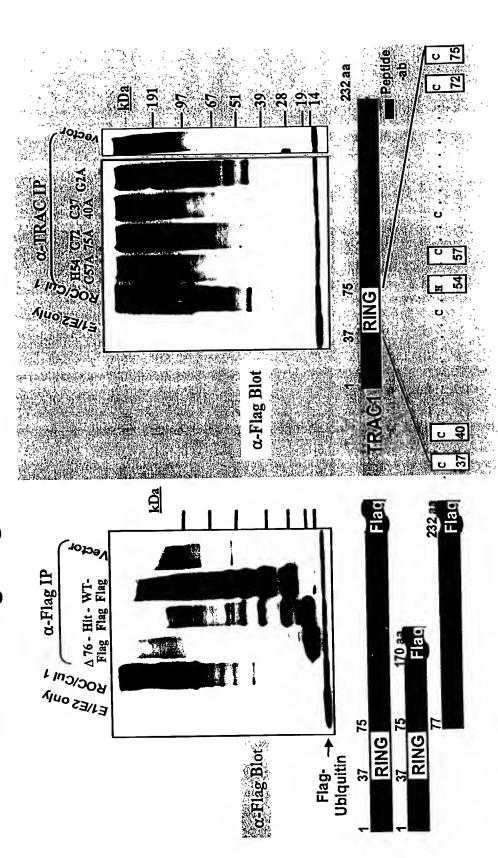


pEFnig/Ring finger point mutants: H54A, C75A, C37, 40A, H54C57A, C72, 75A The following expression plasmids were generated: pEFnig/Myristylation site mutant: G2A

FIG. 13A.

Figure 13B

TRAC1 Ring-finger Domain Disrupt Ligase Activity Point mutations in Conserved Residues of the



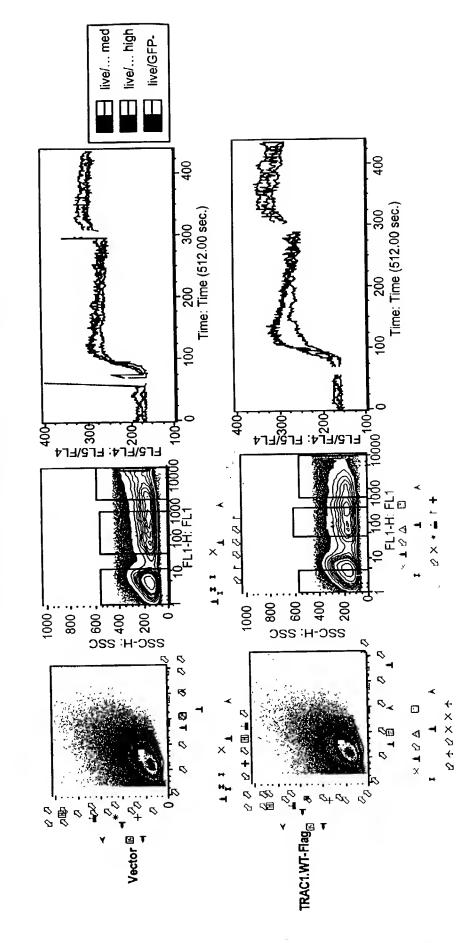
H uh7 TRAC1/HuPO HMAC Expression of TRAC-1 mRNA is ~8 fold higher in PBMC than in Jurkat cells Hela A 549 PhoenixA PBM C BJAB Jurkat 8.0 0.0 7.0 Relative expression

Figure 14

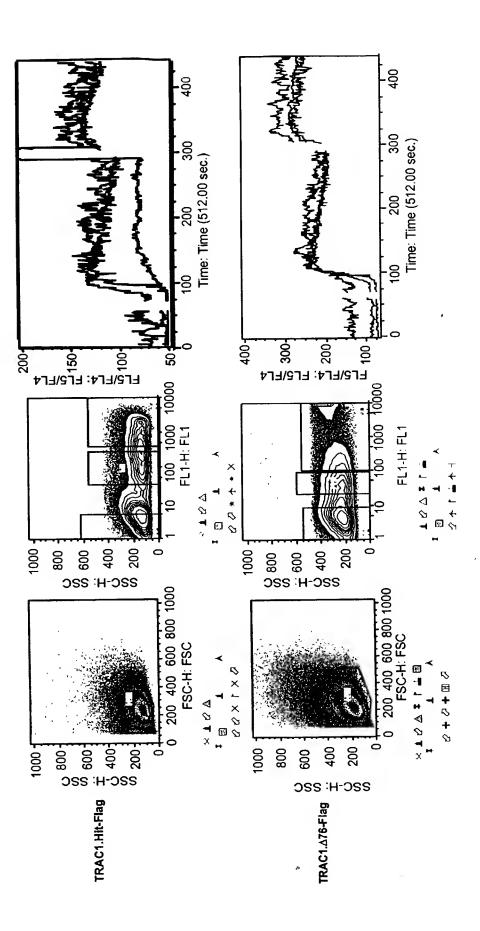
1

13

Figure 15A
C-terminal Truncated TRAC1 Blocks
TCR-induced Ca<sup>2+</sup> Influx







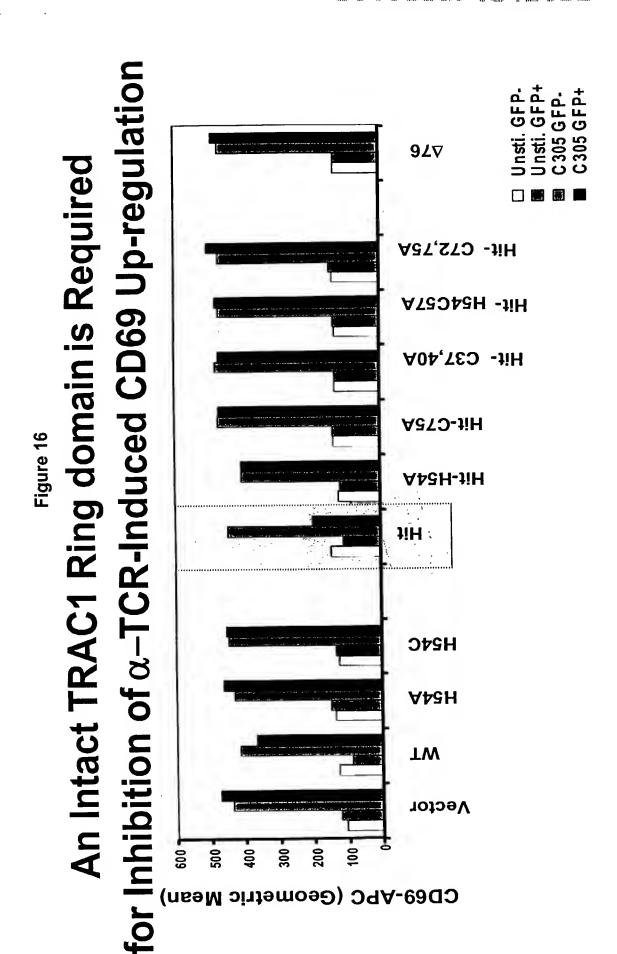


Figure 17

.. :1

## Summary of Functional Effects by Different TRAC-1 constructs

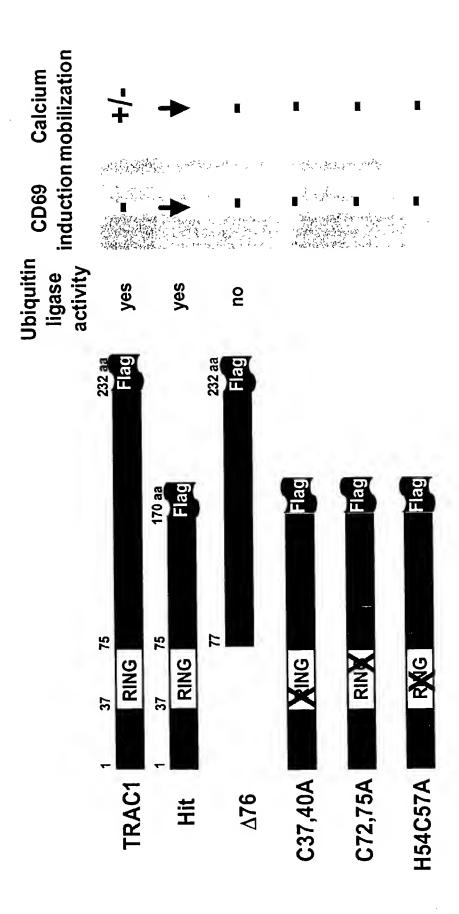


Figure 18

Transiently Transfected TRAC1 Protein Binds to Ubiquitin -Conjugating Enzymes (E2s) UbcH7 and UbcH5 in vitro

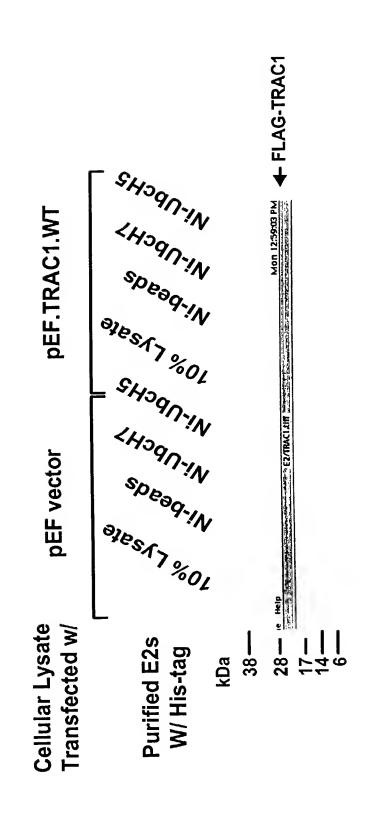


Figure 19

## Model for TRAC-1 regulation of T cel activation

